Amendment to the Claims

1. (Currently amended) A method of ~~diagnosing an increased probability of~~ screening for breast cancer in a subject, the method comprising obtaining a sample containing cells from the subject, comparing the ~~expression pattern~~ level of ~~CXCL9 or~~ FLJ20174, SEQ ID NO:3 or SEQ ID NO:4 nucleic acid ~~or gene product~~ in ~~a~~ the sample from ~~a~~ the subject with the ~~expression pattern~~ level of ~~CXCL9 or~~ FLJ20174, SEQ ID NO:3 or SEQ ID NO:4 nucleic acid ~~or gene product~~ in one or more control samples from one or more non-cancerous breast tissues, wherein ~~an upregulation~~ a significant increase in the ~~expression pattern of CXCL9 or~~ level of FLJ20174, SEQ ID NO:3 or SEQ ID NO:4 in the subject sample compared to the control samples is indicative of ~~an increased probability of~~ breast ~~or ovarian~~ cancer in the subject.

2. (Canceled)

3. (Currently amended) The method of claim ~~2~~ 1, wherein the one or more control breast tissue samples from a non-cancerous breast tissue are also derived from the subject.

4. (Canceled)

5. (Currently amended) The method of claim [[4]] 1, wherein the difference in the ~~expression pattern~~ level is an ~~upregulation~~ increase of at least two fold over the level of ~~expression of CXCL9 or~~ FLJ20174, SEQ ID NO:3 or SEQ ID NO:4 nucleic acid in the one or more non-cancerous breast tissue samples.

6. (Canceled)

7. (Currently amended) The method of claim [[6]] 1, wherein the cells are obtained from breast ~~or ovarian~~ tissue.

8. (Currently amended) The method of claim 1, wherein the subject sample comprises serum, nipple aspirate or ductal fluid obtained from the subject.

9. (Currently amended) The method of claim 1, wherein the ~~expression pattern~~ level of ~~CXCL9 or~~ FLJ20174, SEQ ID NO:3 or SEQ ID NO:4 is determined by ~~detecting the presence in~~ assaying the sample ~~of a nucleic acid comprising~~ with a probe or primer consisting of 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30 or more contiguous nucleotides of ~~SEQ ID NO:1~~ SEQ ID NO:3 or SEQ ID NO:4, or the complement thereof.

10. (Currently amended) The method of claim ~~9~~ 1, wherein the subject nucleic acid is an mRNA or hnRNA.

11. (Currently amended) The method of claim ~~9~~ 1, wherein the nucleic acid in the subject sample is a cDNA.

12. (Currently amended) The method of claim 9, wherein the step of ~~detecting further~~ assaying comprises amplifying the nucleic acid.

13.-65 (Canceled)

66. (New) The method of claim 9, wherein the step of assaying comprises a polymerase chain reaction step.

67. (New) The method of claim 9, wherein the step of assaying comprises a reverse transcriptase polymerase chain reaction step.

68. (New) The method of claim 9, wherein the step of assaying comprises a DNA to DNA hybridization step.

69. (New) The method of claim 9, wherein the step of assaying comprises a DNA to RNA hybridization step.

70. (New) The method of claim 9, wherein the step of assaying comprises a single stranded conformational polymorphism analysis.

71. (New) The method of claim 9, wherein the step of assaying wherein the probe is affixed to a solid support.

72. (New) The method of claim 71, wherein the solid support is a membrane, a microtiter plate, or a polystyrene bead.

73. (New) The method of claim 9, wherein the step of assaying comprises fluorescent in situ hybridization.

74. (New) The method of claim 9, wherein the step of assaying comprises a molecular beacon assay.